

1/35
SEQUENCE LISTING

5 <110> Biotica Technology Limited
 Pfizer Inc
 Gaisser, Sabine

10 <120> Polyketides and their synthesis
 <130> IP0013-WO01
 <150> GB0327721.7
 <151> 2003-11-28

15 <160> 57
 <170> PatentIn version 3.2

20 <210> 1
 <211> 305
 <212> PRT
 <213> Streptomyces fradiae

<400> 1

25 Met Asn Asp Arg Pro Arg Arg Ala Met Lys Gly Ile Ile Leu Ala Gly
 1 5 10 15

30 Gly Ser Gly Thr Arg Leu Arg Pro Leu Thr Gly Thr Leu Ser Lys Gln
 20 25 30

35 Leu Leu Pro Val Tyr Asp Lys Pro Met Ile Tyr Tyr Pro Leu Ser Val
 35 40 45

40 Leu Met Leu Ala Gly Ile Arg Glu Ile Gln Ile Ile Ser Ser Lys Asp
 50 55 60

45 His Leu Asp Leu Phe Arg Ser Leu Leu Gly Glu Gly Asp Arg Leu Gly
 65 70 75 80

50 Leu Ser Ile Ser Tyr Ala Glu Gln Arg Glu Pro Arg Gly Ile Ala Glu
 85 90 95

55 Ala Phe Leu Ile Gly Ala Arg His Ile Gly Gly Asp Asp Ala Ala Leu
 100 105 110

60 Ile Leu Gly Asp Asn Val Phe His Gly Pro Gly Phe Ser Ser Val Leu
 115 120 125

Thr Gly Thr Val Ala Arg Leu Asp Gly Cys Glu Leu Phe Gly Tyr Pro
 130 135 140

Val Lys Asp Ala His Arg Tyr Gly Val Gly Glu Ile Asp Ser Gly Gly

2/35

	145		150		155		160									
5	Arg	Leu	Leu	Ser	Leu	Glu	Glu	Lys	Pro	Arg	Arg	Pro	Arg	Ser	Asn	Leu
					165					170					175	
10	Ala	Val	Thr	Gly	Leu	Tyr	Leu	Tyr	Thr	Asn	Asp	Val	Val	Glu	Ile	Ala
				180					185					190		
15	Arg	Thr	Ile	Ser	Pro	Ser	Ala	Arg	Gly	Glu	Leu	Glu	Ile	Thr	Asp	Val
			195					200					205			
20	Asn	Lys	Val	Tyr	Leu	Glu	Gln	Gly	Arg	Ala	Arg	Leu	Thr	Glu	Leu	Gly
		210					215					220				
25	Arg	Gly	Phe	Ala	Trp	Leu	Asp	Met	Gly	Thr	His	Asp	Ser	Leu	Leu	Gln
	225					230					235					240
30	Ala	Gly	Gln	Tyr	Val	Gln	Leu	Leu	Glu	Gln	Arg	Gln	Gly	Glu	Arg	Ile
					245					250					255	
35	Ala	Cys	Ile	Glu	Glu	Ile	Ala	Met	Arg	Met	Gly	Phe	Ile	Ser	Ala	Glu
				260					265					270		
40	Gln	Cys	Tyr	Arg	Leu	Gly	Gln	Glu	Leu	Arg	Ser	Ser	Ser	Tyr	Gly	Ser
			275					280					285			
45	Tyr	Ile	Ile	Asp	Val	Ala	Met	Arg	Gly	Ala	Ala	Ala	Asp	Ser	Arg	Ala
		290					295					300				
50	Gln															
	305															
55	<210>	2														
	<211>	303														
	<212>	PRT														
	<213>	Streptomyces fradiae														
60	<400>	2														
	Met	Asn	Asp	Arg	Pro	Arg	Arg	Ala	Met	Lys	Gly	Ile	Ile	Leu	Ala	Gly
	1				5					10				15		
65	Gly	Ser	Gly	Thr	Arg	Leu	Arg	Pro	Leu	Thr	Gly	Thr	Leu	Ser	Lys	Gln
				20					25					30		
70	Leu	Leu	Pro	Val	Tyr	Asp	Lys	Pro	Met	Ile	Tyr	Tyr	Pro	Leu	Ser	Val
			35					40					45			

3/35

Leu Met Leu Ala Gly Ile Arg Glu Ile Gln Ile Ile Ser Ser Lys Asp
 50 55 60

5

His Leu Asp Leu Phe Arg Ser Leu Leu Gly Glu Gly Asp Arg Leu Gly
 65 70 75 80

10

Leu Ser Ile Ser Tyr Ala Glu Gln Arg Glu Pro Arg Gly Ile Ala Glu
 85 90 95

15

Ala Phe Leu Ile Gly Ala Arg His Ile Gly Gly Asp Asp Ala Ala Leu
 100 105 110

20

Ile Leu Gly Asp Asn Val Phe His Gly Pro Gly Phe Ser Ser Val Leu
 115 120 125

25

Thr Gly Thr Val Ala Arg Leu Asp Gly Cys Glu Leu Phe Gly Tyr Pro
 130 135 140

30

Val Lys Asp Ala His Arg Tyr Gly Val Gly Glu Ile Asp Ser Gly Gly
 145 150 155 160

35

Arg Leu Leu Ser Leu Glu Glu Lys Pro Arg Arg Pro Leu Glu Pro Gly
 165 170 175

40

Arg His Arg Leu Tyr Leu Tyr Thr Asn Asp Val Val Glu Ile Ala Arg
 180 185 190

45

Thr Ile Ser Pro Ser Ala Arg Gly Glu Leu Glu Ile Thr Asp Val Asn
 195 200 205

50

Lys Val Tyr Leu Glu Gln Gly Arg Ala Ala His Gly Ala Gly Ala Val
 210 215 220

55

Val Ala Trp Leu Asp Met Gly Thr His Asp Ser Leu Leu Gln Ala Gly
 225 230 235 240

60

Gln Tyr Val Gln Leu Leu Glu Gln Arg Gln Gly Glu Arg Ile Ala Cys
 245 250 255

65

Ile Glu Glu Ile Ala Met Arg Met Gly Phe Ile Ser Ala Glu Gln Cys
 260 265 270

70

Tyr Arg Leu Gly Gln Glu Leu Arg Ser Ser Ser Tyr Gly Ser Tyr Ile
 275 280 285

4/35

Ile Asp Val Ala Met Arg Gly Ala Ala Ala Asp Ser Arg Ala Gln
 290 295 300

5 <210> 3
 <211> 333
 <212> PRT
 <213> Streptomyces fradiae

10 <400> 3

Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Phe
 1 5 10 15

15 Thr Gly Gln Leu Leu Thr Gly Ala Tyr Pro Asp Leu Gly Ala Thr Arg
 20 25 30

20 Thr Val Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Pro Ala Asn Leu
 35 40 45

25 Glu His Val Ala Gly His Pro Asp Leu Glu Phe Val Arg Gly Asp Ile
 50 55 60

30 Ala Asp Gln Ala Leu Val Arg Arg Leu Met Glu Gly Val Gly Leu Val
 65 70 75 80

Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Glu Ser Ser
 85 90 95

35 Glu Ala Phe Val Arg Thr Asn Val Glu Gly Thr Arg Val Leu Leu Gln
 100 105 110

40 Ala Ala Val Asp Ala Gly Val Gly Arg Phe Val His Ile Ser Thr Asp
 115 120 125

45 Glu Val Tyr Gly Ser Ile Ala Glu Gly Ser Trp Pro Glu Asp His Pro
 130 135 140

50 Leu Ala Pro Asn Ser Pro Tyr Ala Ala Thr Lys Ala Ala Ser Asp Leu
 145 150 155 160

Leu Ala Leu Ala Tyr His Arg Thr Tyr Gly Leu Asp Val Arg Val Thr
 165 170 175

55 Arg Cys Ser Asn Asn Tyr Gly Pro Arg Gln Tyr Pro Glu Lys Ala Val
 180 185 190

60 Pro Leu Phe Thr Thr Asn Leu Leu Asp Gly Leu Pro Val Pro Leu Tyr
 195 200 205

5/35

5 Gly Asp Gly Gly Asn Thr Arg Glu Trp Leu His Val Asp Asp His Cys
 210 215 220
 Arg Gly Val Ala Leu Val Ala Ala Gly Gly Arg Pro Gly Val Ile Tyr
 225 230 235 240
 10 Asn Ile Gly Gly Gly Thr Glu Leu Thr Asn Ala Glu Leu Thr Asp Arg
 245 250 255
 15 Ile Leu Glu Leu Cys Gly Ala Asp Arg Ser Ala Val Arg Arg Val Ala
 260 265 270
 20 Asp Arg Pro Gly His Asp Arg Arg Tyr Ser Val Asp Thr Thr Lys Ile
 275 280 285
 25 Arg Glu Glu Leu Gly Tyr Ala Pro Arg Thr Gly Ile Thr Glu Gly Leu
 290 295 300
 Ala Gly Thr Val Ala Trp Tyr Arg Asp Asn Arg Ala Trp Trp Glu Pro
 305 310 315 320
 30 Leu Lys Arg Ser Pro Gly Gly Arg Glu Leu Glu Arg Ala
 325 330
 35 <210> 4
 <211> 333
 <212> PRT
 <213> Streptomyces fradiae
 40 <400> 4
 Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Phe
 1 5 10 15
 45 Thr Gly Gln Leu Leu Thr Gly Ala Tyr Pro Asp Leu Gly Ala Thr Arg
 20 25 30
 50 Thr Val Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Pro Ala Asn Leu
 35 40 45
 55 Glu His Val Ala Gly His Pro Asp Leu Glu Phe Val Arg Gly Asp Ile
 50 55 60
 60 Ala Asp His Gly Trp Trp Arg Arg Leu Met Glu Gly Val Gly Leu Val
 65 70 75 80

6/35

	Val	His	Phe	Ala	Ala	Glu	Ser	His	Val	Asp	Arg	Ser	Ile	Glu	Ser	Ser	85	90	95
5	Glu	Ala	Phe	Val	Arg	Thr	Asn	Val	Glu	Gly	Thr	Arg	Val	Leu	Leu	Gln	100	105	110
10	Ala	Ala	Val	Asp	Ala	Gly	Val	Gly	Arg	Phe	Val	His	Ile	Ser	Thr	Asp	115	120	125
15	Glu	Val	Tyr	Gly	Ser	Ile	Ala	Glu	Gly	Ser	Trp	Pro	Glu	Asp	His	Pro	130	135	140
20	Val	Ala	Pro	Asn	Ser	Pro	Tyr	Ala	Ala	Thr	Lys	Ala	Ala	Ser	Asp	Leu	145	150	155
	Leu	Ala	Leu	Ala	Tyr	His	Arg	Thr	Tyr	Gly	Leu	Asp	Val	Arg	Val	Thr	165	170	175
25	Arg	Cys	Ser	Asn	Asn	Tyr	Gly	Pro	Arg	Gln	Tyr	Pro	Glu	Lys	Ala	Val	180	185	190
30	Pro	Leu	Phe	Thr	Thr	Asn	Leu	Leu	Asp	Gly	Leu	Pro	Val	Pro	Leu	Tyr	195	200	205
35	Gly	Asp	Gly	Gly	Asn	Thr	Arg	Glu	Trp	Leu	His	Val	Asp	Asp	His	Cys	210	215	220
40	Arg	Gly	Val	Ala	Leu	Val	Gly	Ala	Gly	Gly	Arg	Pro	Gly	Val	Ile	Tyr	225	230	235
	Asn	Ile	Gly	Gly	Gly	Thr	Glu	Leu	Thr	Asn	Ala	Glu	Leu	Thr	Asp	Arg	245	250	255
45	Ile	Leu	Glu	Leu	Cys	Gly	Ala	Asp	Arg	Ser	Ala	Leu	Arg	Arg	Val	Ala	260	265	270
50	Asp	Arg	Pro	Gly	His	Asp	Arg	Arg	Tyr	Ser	Val	Asp	Thr	Thr	Lys	Ile	275	280	285
55	Arg	Glu	Glu	Leu	Gly	Tyr	Ala	Pro	Arg	Thr	Gly	Ile	Thr	Glu	Gly	Leu	290	295	300
	Ala	Gly	Thr	Val	Ala	Trp	Tyr	Arg	Asp	Asn	Arg	Ala	Trp	Trp	Glu	Pro	305	310	315
50	Leu	Lys	Arg	Ser	Pro	Gly	Gly	Arg	Glu	Leu	Glu	Arg	Ala						

7/35
330

325

5 <210> 5
 <211> 2160
 <212> DNA
 <213> Streptomyces eurythermus

10 <400> 5
 ggc atgcctt cgggggtgtgc ggcgggcgcct cagagcgtgg ccagtaacctc gtgcagggcc 60
 gcgatcacct tgtcctgtac gtccgggcgcg agccccgggt acatcggcag cgagaagatc 120
 15 tcgtccgcca gccgctccgt caccggcagc gagcccttgg cgtaccccag gtgcgcgaag 180
 cccgtcatgg tgtgcacggg ccacgggtaa ctgatgttga gcgagatccc gtacgacttg 240
 agcgcctcga tgatgtcgtc ccggcgcggg tggcggacga cgtacacgta atacacgtgg 300
 20 tcgttgcctt cgggtgacgga cggcagcacc aggcgcgcgg ggcccgtcag gttcgcgagt 360
 ccttcggcgt aacgccgggc gaccgcgcgc cggccctcga tgtagcggtc gaggcgggtg 420
 agcttgccgc gcaggatctc cgcctgcacc tcgtcgagcc ggctgttgtg gccgggcgtc 480
 25 tgcacgacgt agtacacgtc ctocatgccg tagtagcgca gccggcgag cgcaaggctc 540
 acgtccgcgt cgtcggtcag cacggccccg ccgtcgccgt acgcaccgag gaccttcgtc 600
 30 gggtagaacg agaaggcggc ggcgtcgccc agcgtgccgg ccagctcgcc gtggtggcgg 660
 gcaccgtgcg cctggggcgca gtccctccagc accaccaggc cgtgctgctc ggccagggcg 720
 cgcaagggcg ccatgtcgac gcaactgccg tacagggtgca ccggcagcag ggccttcgtg 780
 35 cgcgggggtga tgacgtccgc gacctggctg gtgtccatga ggtggtcctc ggcgcggaag 840
 tcgacgaaga cgggcgtggc accgggtgccg tcgatggcca ccaccgtcg cgcgggcgtg 900
 40 ttggagacgg tgacgacctc gtcccccggg cccaccccga gcgcctgcag accagcttg 960
 acggcggttg tgccgttgtc gacaccgcgc cagtggcgca ggccgtggta gtccgcgaac 1020
 45 tccttctcga acccgccac gctggggccg aggaccaact gcccgaggc gaagacggtc 1080
 tcgacggcgt cgaggaggtc cgcgcgttcg ttctggtatt ccgccaggta gtcccagacg 1140
 taggtagtca cggagagctc aacctccaga gtgtttcgat ggggtggtgg gaagccggtg 1200
 50 cgcgcggacc aggtcgtgcc agcagtcgcg gaccgactcc cgcagcgaac ggcgcgggtg 1260
 ccagcccagc agggcgcgcg ccgcgcgggt gtgcacccgc agccagtcct cccgggtgcc 1320
 55 gggagcccgg cccggagccg ggcgctccac caccgcgcgc ggaatgccgc tcgcctcgat 1380
 gaacaggccg accaggtcgc ggacggcgac cgcctcgccc cgcggatgc cgacggcgac 1440
 cgggacggcc ggtgcgcggg cggcggccac gacggcgctg gccacgtccc gcacatcgac 1500
 60 gtagtcccgg tgcgcgcgca gccgggacag ttccacgacg gcctccgcac ccgtcccggc 1560

8/35

ggccgcacagc agccgctcgg cgacctggcc cagcagactg atccgcgggg tgccggggcc 1620
 cgacacgttg gacacccgta gcaccacacc gtcgacccac ccgcccagagg tgccccgcag 1680
 5 caccgcctcg ctggcgggcga gcttgctcct gccgtacgcc gtgtccgggc gcggtacggc 1740
 gtcggcgccc accgaaccgc cgggcgtcac cgggccgtac tccagtaccg agccgaggtg 1800
 10 gaccagccgc ggccgcgcgg acatcagcgc cagcgcctcc agcaggcgca gcgtgggcac 1860
 cgcggtggcg gaccacatct gctcgtcggg acggccccag atgottccga cggagttgac 1920
 gatcgtgtcc ggacgctccg cgtccagggc ggccggccagc gccgcgggat ccgtaccggc 1980
 15 cagggtccagg gtgacgcagc ggtacggcat cggctcctcg ggccggcggc ggcccaccac 2040
 caccacgtca cggccccgcg cggcgaacgc cgcgcacaca tgccggccga cgtaccggc 2100
 20 gccgcccagg accacgacgc tgccactgcc actgccgcgc ggcacgggat cgttcaccat 2160
 <210> 6
 <211> 4461
 <212> DNA
 25 <213> *Streptomyces eurythermus*
 <400> 6
 cgtcagtaca gcgtgtgggc acacgccacc aggggtgcgca gctcgatgtt gaggtagttg 60
 30 ccgtgcgcca gcagcccggg gagctgaccg agcgacagcc aggcgaagtc gtccggtgcg 120
 tcctccggga agtcgtgcgg gacctccacg atcacgtagc ggttctgggc gtggaagaag 180
 35 cgcccgccct cctcggactg gacggcgctc tagcgcacgt cctgaggcgg ccgggacagc 240
 acgtcctcca ggtacggcgg gccgggcagc ccccgcgga cgggtgtgctc ctgtggccgg 300
 cactggaccg tggggggccag ctccggcgacg ttcagggtgcc cgacgtccac ccgtgccgc 360
 40 acgagcgcgt gcagcacgcc gtcgacggac ttgaccagca gcgccatcag acccggcagc 420
 cgcggtcga tgagcggctg cgtccaggag gtgacctccc ggtgctggc gctgacctc 480
 45 gcggccatga cccggaagtg ccgccgcgtc tcgtgggcga tctcgtgcgg cgtgcggtac 540
 cagccgtccg ccgtcaccgt atcgagcggc acccggttct gcaccagctc ccgcagggcg 600
 cgcacacccg tgaaccacgt caggacctcg gccgtcgtgt gccgcgccgc acccggcgag 660
 50 ccgaagaagg agcgcagcac gggggacggg gcggacgcgt cggcgtccgc cgtgggcagg 720
 caggcgagga tggaccgggc gtccatgttg accacgttgt ccagcatcag cagccggcgg 780
 55 agctgcccca gcgtcagcca gcggaagtcc tccccgatgt cgaggtcgtc gtccgccgcc 840
 aactcgacga tcatgttccg gttgcgtttg gccaggaacc agtcgcctg ttcggactgg 900
 atcgagtga ccaggacacg cggccgtcgc ggcccatga acagggtccag atagcggatg 960
 60 tcgcgccccc ggtgcacccc ggtgaagttg ctccgggtgg cctgcacggt cggcgacacc 1020

9/35

	tgaagaacgt	tgacgttccc	gggctccatc	ttggcctgca	tcaggaagtg	cagcaccocg	1080
	tcgatctccc	gcgccacgat	cccgagcagc	cccacctccg	gctgcacgat	gatgggctgc	1140
5	gtccagcccc	gctcgggcag	cgggtccgta	cggacgtgca	gcccctccac	ggagaagaaa	1200
	cggcccgaacg	cgtggtgcag	gtttcccgta	cccgggtgga	agctccagcc	gcgcagctcc	1260
10	gcgaagggaa	cgcgggacac	gtcgaagcgc	cccgcccgca	ggcgttcggc	cagccagccg	1320
	gagatgccgt	cgaacggcgt	gaccgcactg	tccgcggtgc	gtgccgacac	cagcaccocg	1380
	cgcgccgtgt	ccaccgggtc	accgggcggg	accgcgtccg	cacggcgccg	cgcggcgccg	1440
15	tgcggggcgg	gggcggatcg	cggcggtacg	ggttcgcggg	cgggtgtccg	ggcgggtgcg	1500
	ggcgggacgg	ggccggtgct	cgtgtccgcg	gcggtacgcg	gtgggacggg	cccgggtggc	1560
20	gtgtccgcgg	tggccgtgcc	ggcgagggcg	tcgccgatgg	tccggcacac	ctcgtccatc	1620
	cggtcgttca	gatagaagtg	accgccggcg	aagggtgtgca	gggcgaaggg	gcccgtggtc	1680
	agctcccgc	aggccctcgc	ctcctccagc	gggacatcgg	gatcacggtc	accggtgagc	1740
25	accgtgaccg	gacagtccag	cgcaccgcgc	ggcacatacg	cgtacgtgcc	cgcgcgcccg	1800
	tagtcgttgc	ggatcgccgg	cagggccagc	cgcagcagct	cctcgtcctg	gaggacggcg	1860
30	tcctcgggtg	cctgaagcgt	ggcgatctcc	gcgatcagcg	cgtcgtcgtc	gaggaggtgg	1920
	gcgacgtccc	gccggcgcac	cgtcggcgca	cggcgggccc	acaccagcag	atggacgggg	1980
	gaggcctgcc	cggaaaccgc	cagccggcgc	gcgacctcga	acgccaccgt	ggcaccatg	2040
35	ctgtgcccga	acagcgcgag	cggacggtcg	gcccagcgca	ggatctccgg	caccacctgg	2100
	tccaccaggc	cogatatgga	cgggatgaac	ggctcgtgcc	ggcggtcctg	gcggcccggg	2160
40	tactgcaccg	ccagcgcctc	cacgggtctc	tccagtccgc	gtgccagggc	ggcgaaggag	2220
	gtcgcggcgc	caccggcgtg	cgggaagcag	accagaogca	gttccggatc	ccgcaccggg	2280
	cggtaacggc	ggacccacag	accctcgtcc	gggtgtccgg	ccggcgacgg	ggctcccggg	2340
45	acgggtggtg	cggaaagggg	gctcacggcg	gatccagctc	ctcgcggtcg	gggggaccgc	2400
	tgtcggggac	ggcacgtcgg	gtgcggacgt	cgggtacggg	cgtcggggcg	tgacggggag	2460
50	ggacggggcg	gtcgggtcagt	cgggtgcgcg	ggcctcctgc	gcggccttct	tcagcggttc	2520
	ccaccacgcg	cggttctccg	cgtaccagcg	caccgtgtcc	gccaggcccc	tcgtgaagtc	2580
	cgtacgcggg	gcatagccca	gctcggccgt	gatcttgccg	atgtccagcg	cgtaccgcag	2640
55	gtcgtgcccc	ggccgggtcg	cgacgtggcg	caccgacgag	gcgtcggcac	cgcacagccc	2700
	gagcagccgc	ttcgtcagct	cccggttggg	cagctccgtc	ccgccaccga	tgtggtagac	2760
60	ctcggccggg	cgcgcgcggg	tcgccaccag	gctgatcccg	cggcagtggt	cgtccacgtg	2820
	cagccagtcc	cggctgttgc	cgcgcgtcgt	gtacagcggc	accgtcagac	cgtccaacag	2880

10/35

5 gtctgtggcg aagagcggga cgaccttctc ggggtgctgg tacgggocgt agttgttgga 2940
 gcaccgggtg acgacgaccg gcaggccgta cgtccgggtg taggccagcg ccaggaggtc 3000
 cgacgcgcgc ttcgaggcgg cgtacgggga gttcggcgcc agcggctgct cctcgcgcca 3060
 cgacccctcg gcgacgagc cgtacacctc gtccgtggag acgtggacga accggccggc 3120
 10 ccccgctcc accgcggcct gcaagaggac ttgctcccc cgtacgttcg tctcgacgaa 3180
 cgccgacgcg tcggcgatgg agcgggtccac gtgcgactcc gccgcgaagt ggaccacgac 3240
 gtccgcccc cgcacgaccc gggacatcac ctccgcgtcc cggatgtcgg cgtgcacgaa 3300
 15 ctccagcgac ggatgggtcc cgaccgggtc caggttggcg aggttcccg cataggtcag 3360
 cttgtcgacc accaccgtcc gcgccccggc cagggtccgga tacgccccgg ccagcagttg 3420
 20 tctgacgaag tgcgagccga tgaagccgc acctccgtg accagcagcc gcatgggagc 3480
 acagaccttt ctccagga cgggaaacgg ggaggcggac ggggacggag gcgagggcgg 3540
 tggctatgcg gccgggtccg acatgagggt ctccgccacg tccatcaagt accggccgta 3600
 25 gctggagctc tcgagttcac ggcgagctc gtggcactgc cgcgcgtga tgtaccccat 3660
 ccgcagggcg atctcctcga cgcaggagat ccgcacgcc tgccgctgct ccaggagctg 3720
 30 gacgtactgc cccgcttgca gcagcgagct gtgcgtgcc atgtccagcc aggcgaaccc 3780
 gcgccccagt tccgtcatac gggcgcgcc ctgctccagg tacaccttgt tgacgtcgg 3840
 gatctccagc tcgcccccg gcgacgggtg cagccgccc gcgatgtcca ccacgcggtt 3900
 35 gtcgtagaag tacagcccc tcaccgcgag atgggagcgg ggcttctccg gcttctctc 3960
 cagggacacc agcgggcctt ccgcgtcgac ctgcgcgac ccgtagcgcc gggggtcctt 4020
 40 caccgggtag ccgaacagct cgcagccgtc cagccgcgc gcggtggagg ccagcacgga 4080
 ggagaacccc ggaaccgtga agacgttgtc cccaggatg agggcgaccg ggtcgtcccc 4140
 gatgtgctcc tcgccgatga ggaacgcctc ggcgatgcc cggggctcct cctgctcggc 4200
 45 gtagccgaca ctgatccga tgcggctgcc gtgcgccagc agcgaacgga acatctccaa 4260
 gtgcgtcttc gacgtgatga tctggatgtc ccggatcccc gccagcatga gcaccgacag 4320
 50 cgggtagtag atcatgggct tgcgtagac cggcagcaac tgcttgga gtgccccggt 4380
 cagggggcgc aggcgcgtgc cgtgcgcc cgcaggatg atgcccttca tggggcgcgcg 4440
 55 gtcgcgcgtc gtcttcgtca t 4461

60 <210> 7
 <211> 3375
 <212> DNA
 <213> Streptomyces eurythermus

11/35

<400> 7
 gtgagccccc caccgcgcac cgaggaccgc gcgcgcgcgc ggcgccgcct gcaactgacc 60
 5 cgcgagagccc agtgggttcgc gggaacccag gacgacccgt acgcgctcgt cctgcgcgcc 120
 gaggccaccg acccggcccc gtacgaggag cggatccggg cccacggggc gctcttccgc 180
 agcgacctgc tcgacacctg ggtcacggcg agcagggccg tcgccgacga agtgatcacc 240
 10 tcaccgcctt tcgacgggct cacggccgac gggcggcgcc ccggcgcgcg ggaactgccg 300
 ctgtccggca ccgcgctcga cgcggaccgc gccacatgcg cacggttcgg ggccctcacc 360
 15 gcctggggcg ggccgctgct gccggcgccg cagcagcggg cgctgcgcga gtccgccgaa 420
 cggcgggccc acacactcct cgacggggcg gaggcgcgcc tggccgccga cggcacccgtc 480
 gacctcgtcg acgcgtacgc ccgcaggctc cccgcgctgg tcctccgcga acagctcggc 540
 20 gtgccggagg aggcggcgac cgccttcgag gacgcgctgg ccggctgccg ccgcaccctg 600
 gacggcgccc tgtgcccgca actcctcccg gacgcgctgg cgggggtgcg cgcggaagcc 660
 25 gcgctgaccg ccgtgctggc ctccgccctg cgcgggactc cggccggccg ggcccccgac 720
 gccgtcgccg ccgcgccgac cctggccgct gcggccgcgc agcccgagc caccctcgtc 780
 ggcaacgcgc tacaggagct gctggcgcggt cccgcgcagt gggcgagct cgtacgcgac 840
 30 ccgcgcctcg cggccgcgcg ggtgaccgaa acgctgcgtg tcgccccgcc cgtccgcctg 900
 gagcggcggg tcgccccgca ggacacggac atcgccgggc agcgcctccc cgcggggggg 960
 35 agcgtcgtga tcctcgtcgc cgcgctcaac cgcgcgcgcg tatccgcggg aagcgacgcc 1020
 tccaccaccg tccgcgacgc cggcgggccg ccccgtaact ccgccccctc cgtccccctca 1080
 gcccccttcg acctcaccag gcccggtggc gcgcccgggc cgttcgggct ccccggcgac 1140
 40 ctgcacttcc gcctcggcgg gccctgggtc ggaacggctg ccgaagccgc gctcgggtgcg 1200
 ctggccgcac ggctccccgg tctgcgcgcg gcggggccgg ccgtgcggcg ccgcgctca 1260
 ccggtgctgc acggacacgc ccgcctcccc gtgcgcgctg cccggacggc ccgtgacctg 1320
 45 cccgccaccg cacgcgggaa ctgaggaggg agtgccccga tgcgtatcct gctgacgtcg 1380
 ttgcgcgaca acacgcacta ctacaacctg gtccccctcg gctgggcgct gcgcgcgcgc 1440
 50 gggcacgacg tacgggtcgc cagccagccc tcgctgaccg gcaccatcac cggctccggg 1500
 ctgaccgcgc tccccgtggg cgacgacacg gccatcgtcg agctgatcac cgagatcggc 1560
 gacgacctcg tcctctacca gcagggcagt gacttcgtgg acaccgcga cgagccgctg 1620
 55 tcctgggaac acgcctcggg acagcagacg atcatgtcgg ccatgtgctt ctgcgcgctg 1680
 aacggcgaca gcaccatoga cgacatggtg gcgctggccc gttcctggaa accggacctc 1740
 60 gtctctgtgg agcccttcac ctacgcggga cccgtcgccg cgcacgcctg cggcgccgcc 1800

12/35

5 caccgcccggc tgctgtgggg tcccgaactg gtcctcaacg caccggcgga gttcaccggg 1860
 ctgctcgccg agcgccccgt cgaacagcgc gaggaccggg tcggcgaatg gctcacgtgg 1920
 10 acgtctggagc gccacggcct cgcgcgcgac gcggacacga tcgaggaact gttcgccggg 1980
 cagtggacga tcgaccccag cgcgcgggagc ctgcggctgc cggtcgacgg cgaggctgtg 2040
 cccatgcgct tcgtgccgta caacggcgcc tcggctgtcc ccgcctggct ctccgagccg 2100
 cctgcccggc ccgggtcttg cgtcacccctc gggtcttcca cccgggagac ctacggcacg 2160
 gacggcgctc cgttccacga actgctggcc ggactggccg acgtggacgc cgagatcgtc 2220
 15 gccaccctcg acgcggggca gctcccggac gcgcgcggtc tgcccggcaa tgtgcgcgtc 2280
 gtcgacttcg tgccgctgga cgccttgctg ccgagctgcg ccgcgatcgt ccaccacgga 2340
 ggcgcgggaa cctgtttcac ggccaccgtg caccgctcc cgcagatcgt cgtggcctcc 2400
 20 ctctgggacg cgcgcgtgaa ggcgaccaa ctgcgcgagg cgggcgcggg gatcgccctg 2460
 gaccccgggg aactgggctg ggacaccctg cgcggcgccg tcgtgcgggt gctggagagc 2520
 25 cgcgagatgg cgtggcggc gcgtgcctc gcgcacgaga tgctgcgcgc cccaccccg 2580
 gccgcgctcg tccccgcct cgaacgcctc accgcgcgc accgcgcgc ctgatccgc 2640
 caaggagccc ccatgaacct cgaatacagc ggcgacatcg ccggttgta cgacctggtc 2700
 30 caccagggaa agggcaagga ctaccggcg gaggcgagg agctggcgc gcttgtcacc 2760
 cagcgccgc ccggggcccg ctccctctc gacgtggcct gcggaacggg gatgcacctg 2820
 35 cggcacctcg gcgacctctt cgaggagggtg gccgggggtg agatgtcccc cgacatgctg 2880
 gccatcgcg agcgggcgaa ccgggaggcc ggcatccacc ggggggacat gcgggacttc 2940
 40 gccctcgcc gccgcttcca cgcgtgatc tgcatttca gttccatcgg gcacatgcgc 3000
 gaccagcggg aactggacgc ggcatcggc cggttcgcc cgcacctgcc gtccggcggg 3060
 gtcgtgatcg tcgatccctg gtggttccc gagacgttca caccgggta cgtcggcgcg 3120
 45 agcctcgctg aggcgcggg ccgcaccatc gcgcgcttct cccactccgc gctcgaggac 3180
 ggcgcgaccc ggatcgatgt ggactacctc gtcggcgctg cgggggaggg ggtgcggcac 3240
 50 ttgaaggaga cccatcgat cagcctttc gggcgtcgc agtacgaggc ggccttcacc 3300
 gcggcgggga tgtcgtcga gtacctccg cagcgcgca ccgaccgcg actcttcgtc 3360
 ggcgccagg cctga 3375
 55
 <210> 8
 <211> 295
 <212> PRT
 <213> Streptomyces eurythermus
 60
 <400> 8

13/35

Met Lys Gly Ile Ile Leu Ala Gly Gly Ser Gly Thr Arg Leu Arg Pro
 1 5 10 15
 5
 Leu Thr Gly Ala Leu Ser Lys Gln Leu Leu Pro Val Tyr Asp Lys Pro
 20 25 30
 10
 Met Ile Tyr Tyr Pro Leu Ser Val Leu Met Leu Ala Gly Ile Arg Asp
 35 40 45
 15
 Ile Gln Ile Ile Thr Ser Lys Thr His Leu Glu Met Phe Arg Ser Leu
 50 55 60
 20
 Leu Gly Asp Gly Ser Arg Ile Gly Ile Ser Val Gly Tyr Ala Glu Gln
 65 70 75 80
 25
 Glu Glu Pro Arg Gly Ile Ala Glu Ala Phe Leu Ile Gly Glu Glu His
 85 90 95
 30
 Ile Gly Asp Asp Pro Val Ala Leu Ile Leu Gly Asp Asn Val Phe His
 100 105 110
 35
 Gly Pro Gly Phe Ser Ser Val Leu Ala Ser Thr Ala Ala Arg Leu Asp
 115 120 125
 40
 Gly Cys Glu Leu Phe Gly Tyr Pro Val Lys Asp Pro Arg Arg Tyr Gly
 130 135 140
 45
 Val Gly Glu Val Asp Ala Glu Gly Arg Leu Val Ser Leu Glu Glu Lys
 145 150 155 160
 50
 Pro Glu Lys Pro Arg Ser His Leu Ala Val Thr Gly Leu Tyr Phe Tyr
 165 170 175
 55
 Asp Asn Gly Val Val Asp Ile Ala Arg Arg Leu Thr Pro Ser Pro Arg
 180 185 190
 60
 Gly Glu Leu Glu Ile Thr Asp Val Asn Lys Val Tyr Leu Glu Gln Gly
 195 200 205
 65
 Arg Ala Arg Met Thr Glu Leu Gly Arg Gly Phe Ala Trp Leu Asp Met
 210 215 220
 70
 Gly Thr His Ser Ser Leu Leu Gln Ala Gly Gln Tyr Val Gln Leu Leu
 225 230 235 240

14/35

Glu Gln Arg Gln Gly Val Arg Ile Ser Cys Val Glu Glu Ile Ala Leu
 245 250 255

5 Arg Met Gly Tyr Ile Ser Ala Arg Gln Cys His Glu Leu Gly Arg Glu
 260 265 270

10 Leu Glu Ser Ser Ser Tyr Gly Arg Tyr Leu Met Asp Val Ala Glu Thr
 275 280 285

15 Leu Met Ser Gly Pro Ala Ala
 290 295

<210> 9
 <211> 332
 <212> PRT
 20 <213> Streptomyces eurythermus
 <400> 9

25 Met Arg Leu Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Phe
 1 5 10 15

30 Val Arg Gln Leu Leu Ala Gly Ala Tyr Pro Asp Leu Ala Gly Ala Arg
 20 25 30

Thr Val Val Val Asp Lys Leu Thr Tyr Ala Gly Asn Leu Ala Asn Leu
 35 35 40 45

40 Asp Pro Val Ala Asp His Pro Ser Leu Glu Phe Val His Ala Asp Ile
 50 55 60

45 Arg Asp Ala Glu Val Met Ser Arg Val Val Arg Gly Ala Asp Val Val
 65 70 75 80

Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Ala Asp Ala
 85 90 95

50 Ser Ala Phe Val Glu Thr Asn Val Arg Gly Thr Gln Val Leu Leu Gln
 100 105 110

Ala Ala Val Glu Ala Gly Ala Gly Arg Phe Val His Val Ser Thr Asp
 115 120 125

55 Glu Val Tyr Gly Ser Ile Ala Glu Gly Ser Trp Arg Glu Glu Gln Pro
 130 135 140

60 Leu Ala Pro Asn Ser Pro Tyr Ala Ala Ser Lys Ala Ala Ser Asp Leu
 145 150 155 160

15/35

5 Leu Ala Leu Ala Tyr His Arg Thr Tyr Gly Leu Pro Val Val Val Thr
 165 170 175
 Arg Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Pro Glu Lys Val Val
 180 185 190
 10 Pro Leu Phe Ala Thr Asn Leu Leu Asp Gly Leu Thr Val Pro Leu Tyr
 195 200 205
 15 Ser Asp Gly Gly Asn Ser Arg Asp Trp Leu His Val Asp Asp His Cys
 210 215 220
 20 Arg Gly Ile Ser Leu Val Ala Thr Arg Gly Arg Pro Gly Glu Val Tyr
 225 230 235 240
 25 His Ile Gly Gly Gly Thr Glu Leu Thr Asn Arg Glu Leu Thr Lys Arg
 245 250 255
 Leu Leu Gly Leu Cys Gly Ala Asp Ala Ser Ser Val Arg His Val Ala
 260 265 270
 30 Asp Arg Pro Gly His Asp Leu Arg Tyr Ala Leu Asp Ile Gly Lys Ile
 275 280 285
 35 Thr Gly Glu Leu Gly Tyr Ala Pro Arg Thr Asp Phe Thr Thr Gly Leu
 290 295 300
 40 Ala Asp Thr Val Arg Trp Tyr Ala Glu Asn Arg Ala Trp Trp Glu Pro
 305 310 315 320
 45 Leu Lys Lys Ala Ala Gln Glu Ala Arg Arg Thr Asp
 325 330
 <210> 10
 <211> 787
 <212> PRT
 50 <213> Streptomyces eurythermus
 <400> 10
 55 Val Ser Thr Pro Ser Ala Pro Pro Val Pro Gly Ala Pro Ser Pro Ala
 1 5 10 15
 Gly His Pro Asp Glu Gly Leu Trp Val Arg Arg Tyr Arg Pro Val Arg
 20 25 30
 60

16/35

	Asp	Pro	Glu	Leu	Arg	Leu	Val	Cys	Phe	Pro	His	Ala	Gly	Gly	Ala	Ala	
			35					40					45				
5	Thr	Ser	Phe	Ala	Ala	Leu	Ala	Arg	Gly	Leu	Asp	Glu	Thr	Val	Glu	Ala	
		50					55					60					
10	Leu	Ala	Val	Gln	Tyr	Pro	Gly	Arg	Gln	Asp	Arg	Arg	His	Glu	Pro	Phe	
	65					70					75					80	
15	Ile	Pro	Ser	Ile	Ser	Gly	Leu	Val	Asp	Gln	Val	Val	Pro	Glu	Ile	Leu	
				85						90					95		
20	Arg	Trp	Ala	Asp	Arg	Pro	Leu	Ala	Leu	Phe	Gly	His	Ser	Met	Gly	Ala	
				100					105					110			
25	Thr	Val	Ala	Phe	Glu	Val	Ala	Arg	Arg	Leu	Arg	Gly	Ser	Gly	Gln	Ala	
			115					120					125				
30	Ser	Pro	Val	His	Leu	Leu	Val	Ser	Gly	Arg	Arg	Ala	Pro	Thr	Val	Arg	
		130					135					140					
35	Arg	Arg	Asp	Val	Ala	His	Leu	Leu	Asp	Asp	Asp	Ala	Leu	Ile	Ala	Glu	
	145					150					155					160	
40	Ile	Ala	Thr	Leu	Gln	Gly	Thr	Glu	Asp	Ala	Val	Leu	Gln	Asp	Glu	Glu	
				165						170					175		
45	Leu	Leu	Arg	Leu	Ala	Leu	Pro	Ala	Ile	Arg	Asn	Asp	Tyr	Arg	Ala	Ala	
				180					185					190			
50	Gly	Thr	Tyr	Ala	Tyr	Val	Pro	Gly	Gly	Ala	Leu	Asp	Cys	Pro	Val	Thr	
			195					200					205				
55	Val	Leu	Thr	Gly	Asp	Arg	Asp	Pro	Asp	Val	Pro	Leu	Glu	Glu	Ala	Arg	
		210					215					220					
60	Ala	Trp	Arg	Glu	Leu	Thr	Thr	Gly	Pro	Phe	Ala	Leu	His	Thr	Phe	Ala	
	225					230					235					240	
65	Gly	Gly	His	Phe	Tyr	Leu	Asn	Asp	Arg	Met	Asp	Glu	Val	Cys	Arg	Thr	
				245						250					255		
70	Ile	Gly	Asp	Ala	Leu	Ala	Gly	Thr	Ala	Thr	Ala	Asp	Thr	Ala	Thr	Gly	
				260					265					270			
75	Thr	Val	Pro	Pro	Arg	Thr	Ala	Ala	Asp	Thr	Ser	Thr	Gly	Pro	Val	Pro	

17/35

	275		280		285
5	Pro Arg Thr Ala Ala Asp Thr Ala Arg Glu Pro Val Pro Pro Arg Ser 290 295 300				
10	Ala Pro Ala Pro His Gly Ala Ala Arg Arg Arg Ala Asp Ala Val Arg 305 310 315 320				
15	Pro Gly Asp Pro Val Asp Thr Ala Arg Arg Val Leu Val Ser Ala Arg 325 330 335				
20	Thr Ala Asp Ser Ala Val Thr Pro Phe Asp Gly Ile Ser Gly Trp Leu 340 345 350				
25	Ala Glu Arg Leu Arg Ala Gly Arg Phe Asp Val Ser Arg Val Pro Phe 355 360 365				
30	Ala Glu Leu Arg Gly Trp Ser Phe His Pro Gly Thr Gly Asn Leu His 370 375 380				
35	His Ala Ser Gly Arg Phe Phe Ser Val Glu Gly Leu His Val Arg Thr 385 390 395 400				
40	Asp Arg Leu Pro Glu Arg Gly Trp Thr Gln Pro Ile Ile Val Gln Pro 405 410 415				
45	Glu Val Gly Leu Leu Gly Ile Val Ala Arg Glu Ile Asp Gly Val Leu 420 425 430				
50	His Phe Leu Met Gln Ala Lys Met Glu Pro Gly Asn Val Asn Val Leu 435 440 445				
55	Gln Val Ser Pro Thr Val Gln Ala Thr Arg Ser Asn Phe Thr Gly Val 450 455 460				
60	His Arg Gly Arg Asp Ile Arg Tyr Leu Asp Leu Phe Met Gly Pro Arg 465 470 475 480				
	Arg Ala Arg Val Leu Val Asp Ser Ile Gln Ser Glu Gln Ala Asp Trp 485 490 495				
	Phe Leu Ala Lys Arg Asn Arg Asn Met Ile Val Glu Leu Ala Ala Asp 500 505 510				
	Asp Asp Leu Asp Ile Gly Glu Asp Phe Arg Trp Leu Thr Leu Gly Gln 515 520 525				

18/35

5 Leu Arg Arg Leu Leu Met Leu Asp Asn Val Val Asn Met Asp Ala Arg
 530 535 540

Ser Ile Leu Ala Cys Leu Pro Thr Ala Asp Ala Asp Ala Ser Ala Pro
 545 550 555 560

10 Ser Pro Val Leu Arg Ser Phe Phe Gly Ser Pro Gly Ala Ala Arg His
 565 570 575

15 Thr Thr Ala Glu Val Leu Thr Trp Phe Thr Gly Val Arg Ala Leu Arg
 580 585 590

20 Glu Leu Val Gln Asn Arg Val Pro Leu Asp Thr Val Thr Ala Asp Gly
 595 600 605

25 Trp Tyr Arg Thr Pro His Glu Ile Ala His Glu Ser Gly Arg His Phe
 610 615 620

Arg Val Met Ala Ala Glu Val Ser Ala Ser Ser Arg Glu Val Thr Ser
 625 630 635 640

30 Trp Thr Gln Pro Leu Ile Glu Pro Arg Leu Pro Gly Leu Met Ala Leu
 645 650 655

35 Leu Val Lys Ser Val Asp Gly Val Leu His Ala Leu Val Arg Ala Arg
 660 665 670

40 Val Asp Val Gly His Leu Asn Val Ala Glu Leu Ala Pro Thr Val Gln
 675 680 685

45 Cys Arg Pro Gln Glu His Thr Gly Pro Arg Gly Leu Pro Gly Pro Pro
 690 695 700

Tyr Leu Glu Asp Val Leu Ser Ala Pro Pro Gln Asp Val Arg Tyr Asp
 705 710 715 720

50 Ala Val Gln Ser Glu Glu Gly Gly Arg Phe Phe His Ala Gln Asn Arg
 725 730 735

55 Tyr Val Ile Val Glu Val Pro His Asp Phe Pro Glu Asp Ala Pro Asp
 740 745 750

60 Asp Phe Ala Trp Leu Ser Leu Gly Gln Leu Thr Gly Leu Leu Ala His
 755 760 765

19/35

Gly Asn Tyr Leu Asn Ile Glu Leu Arg Thr Leu Val Ala Cys Ala His
 770 775 780

5

Thr Leu Tyr
 785

10

<210> 11
 <211> 333
 <212> PRT
 <213> Streptomyces eurythermus

15

<400> 11
 Met Val Asn Asp Pro Met Pro Arg Gly Ser Gly Ser Gly Ser Val Val
 1 5 10 15

20

Val Leu Gly Gly Ala Gly Tyr Val Gly Arg His Val Cys Ala Ala Phe
 20 25 30

25

Ala Ala Arg Gly Arg Asp Val Val Val Val Gly Arg Arg Pro Pro Glu
 35 40 45

30

Glu Pro Met Pro Tyr Arg Cys Val Thr Leu Asp Leu Ala Gly Thr Asp
 50 55 60

35

Pro Ala Ala Leu Ala Ala Ala Leu Asp Ala Glu Arg Pro Asp Thr Ile
 65 70 75 80

Val Asn Ser Val Gly Ser Ile Trp Gly Arg Thr Asp Glu Gln Met Trp
 85 90 95

40

Ser Ala Thr Ala Val Pro Thr Leu Arg Leu Leu Glu Ala Leu Ala Leu
 100 105 110

45

Met Ser Ala Arg Pro Arg Leu Val His Leu Gly Ser Val Leu Glu Tyr
 115 120 125

50

Gly Pro Val Thr Pro Gly Gly Ser Val Gly Ala Asp Ala Val Pro Arg
 130 135 140

55

Pro Asp Thr Ala Tyr Gly Arg Ser Lys Leu Ala Ala Ser Glu Ala Val
 145 150 155 160

Leu Arg Gly Thr Ser Gly Gly Trp Val Asp Gly Val Val Leu Arg Val
 165 170 175

60

Ser Asn Val Ser Gly Pro Gly Thr Pro Arg Ile Ser Leu Leu Gly Gln

20/35

180

185

190

5 Val Ala Glu Arg Leu Leu Ala Ala Ala Gly Thr Gly Ala Glu Ala Val
 195 200 205

10 Val Glu Leu Ser Arg Leu Arg Ala His Arg Asp Tyr Val Asp Val Arg
 210 215 220

15 Asp Val Ala Asp Ala Val Val Ala Ala Ala Arg Ala Pro Ala Val Pro
 225 230 235 240

Val Ala Val Gly Ile Gly Arg Gly Glu Ala Val Ala Val Arg Asp Leu
 245 250 255

20 Val Gly Leu Phe Ile Glu Ala Ser Gly Ile Pro Ala Arg Val Val Glu
 260 265 270

25 Arg Pro Ala Pro Gly Arg Ala Pro Gly His Arg Glu Asp Trp Leu Arg
 275 280 285

30 Val Asp Thr Gly Ala Ala Arg Ala Leu Leu Gly Trp Ala Pro Arg Arg
 290 295 300

Ser Leu Arg Glu Ser Val Arg Asp Cys Trp His Asp Leu Val Arg Ala
 305 310 315 320

35 His Arg Leu Pro Thr Thr Pro Ser Lys His Ser Gly Gly
 325 330

40 <210> 12
 <211> 373
 <212> PRT
 <213> Streptomyces eurythermus

45 <400> 12

Val Thr Thr Tyr Val Trp Asp Tyr Leu Ala Glu Tyr Gln Asn Glu Arg
 1 5 10 15

50 Ala Asp Leu Leu Asp Ala Val Glu Thr Val Phe Ala Ser Gly Gln Leu
 20 25 30

55 Val Leu Gly Pro Ser Val Asp Gly Phe Glu Lys Glu Phe Ala Asp Tyr
 35 40 45

60 His Gly Leu Arg His Cys Gly Gly Val Asp Asn Gly Thr Asn Ala Val
 50 55 60

21/35

Lys Leu Gly Leu Gln Ala Leu Gly Val Gly Pro Gly Asp Glu Val Val
 65 70 75 80
 5
 Thr Val Ser Asn Thr Ala Ala Pro Thr Val Val Ala Ile Asp Gly Thr
 85 90 95
 10
 Gly Ala Thr Pro Val Phe Val Asp Val Arg Ala Glu Asp His Leu Met
 100 105 110
 15
 Asp Thr Asp Gln Val Ala Asp Val Ile Thr Pro Arg Thr Lys Ala Leu
 115 120 125
 20
 Leu Pro Val His Leu Tyr Gly Gln Cys Val Asp Met Ala Pro Leu Arg
 130 135 140
 25
 Ala Leu Ala Glu Gln His Gly Leu Val Val Leu Glu Asp Cys Ala Gln
 145 150 155 160
 30
 Ala His Gly Ala Arg His His Gly Glu Leu Ala Gly Thr Leu Gly Asp
 165 170 175
 35
 Ala Ala Ala Phe Ser Phe Tyr Pro Thr Lys Val Leu Gly Ala Tyr Gly
 180 185 190
 40
 Asp Gly Gly Ala Val Leu Thr Asp Asp Ala Asp Val Asp Arg Ala Leu
 195 200 205
 Arg Arg Leu Arg Tyr Tyr Gly Met Glu Asp Val Tyr Tyr Val Val Gln
 210 215 220
 45
 Thr Pro Gly His Asn Ser Arg Leu Asp Glu Val Gln Ala Glu Ile Leu
 225 230 235 240
 50
 Arg Arg Lys Leu Thr Arg Leu Asp Arg Tyr Ile Glu Gly Arg Arg Ala
 245 250 255
 55
 Val Ala Arg Arg Tyr Ala Glu Gly Leu Ala Asn Leu Thr Gly Pro Gly
 260 265 270
 60
 Gly Leu Val Leu Pro Ser Val Thr Glu Gly Asn Asp His Val Tyr Tyr
 275 280 285
 Val Tyr Val Val Arg His Pro Arg Arg Asp Asp Ile Ile Glu Ala Leu
 290 295 300

22/35

Lys Ser Tyr Gly Ile Ser Leu Asn Ile Ser Tyr Pro Trp Pro Val His
 305 310 315 320

5 Thr Met Thr Gly Phe Ala His Leu Gly Tyr Ala Lys Gly Ser Leu Pro
 325 330 335

10 Val Thr Glu Arg Leu Ala Asp Glu Ile Phe Ser Leu Pro Met Tyr Pro
 340 345 350

15 Gly Leu Ala Pro Asp Val Gln Asp Lys Val Ile Ala Ala Leu His Glu
 355 360 365

Val Leu Ala Thr Leu
 370

20

<210> 13
 <211> 447
 <212> PRT
 <213> Streptomyces eurythermus

25

<400> 13

Val Ser Pro Ala Pro Ala Thr Glu Asp Pro Ala Ala Ala Gly Arg Arg
 1 5 10 15

30

Leu Gln Leu Thr Arg Ala Ala Gln Trp Phe Ala Gly Thr Gln Asp Asp
 20 25 30

35

Pro Tyr Ala Leu Val Leu Arg Ala Glu Ala Thr Asp Pro Ala Pro Tyr
 35 40 45

40

Glu Glu Arg Ile Arg Ala His Gly Pro Leu Phe Arg Ser Asp Leu Leu
 50 55 60

45

Asp Thr Trp Val Thr Ala Ser Arg Ala Val Ala Asp Glu Val Ile Thr
 65 70 75 80

50

Ser Pro Ala Phe Asp Gly Leu Thr Ala Asp Gly Arg Arg Pro Gly Ala
 85 90 95

Arg Glu Leu Pro Leu Ser Gly Thr Ala Leu Asp Ala Asp Arg Ala Thr
 100 105 110

55

Cys Ala Arg Phe Gly Ala Leu Thr Ala Trp Gly Gly Pro Leu Leu Pro
 115 120 125

60

Ala Pro His Glu Arg Ala Leu Arg Glu Ser Ala Glu Arg Arg Ala His
 130 135 140

23/35

5 Thr Leu Leu Asp Gly Ala Glu Ala Ala Leu Ala Ala Asp Gly Thr Val
 145 150 155 160
 Asp Leu Val Asp Ala Tyr Ala Arg Arg Leu Pro Ala Leu Val Leu Arg
 165 170 175
 10 Glu Gln Leu Gly Val Pro Glu Glu Ala Ala Thr Ala Phe Glu Asp Ala
 180 185 190
 15 Leu Ala Gly Cys Arg Arg Thr Leu Asp Gly Ala Leu Cys Pro Gln Leu
 195 200 205
 20 Leu Pro Asp Ala Val Ala Gly Val Arg Ala Glu Ala Ala Leu Thr Ala
 210 215 220
 25 Val Leu Ala Ser Ala Leu Arg Gly Thr Pro Ala Gly Arg Ala Pro Asp
 225 230 235 240
 Ala Val Ala Ala Ala Arg Thr Leu Ala Val Ala Ala Ala Glu Pro Ala
 245 250 255
 30 Ala Thr Leu Val Gly Asn Ala Val Gln Glu Leu Leu Ala Arg Pro Ala
 260 265 270
 35 Gln Trp Ala Glu Leu Val Arg Asp Pro Arg Leu Ala Ala Ala Ala Val
 275 280 285
 40 Thr Glu Thr Leu Arg Val Ala Pro Pro Val Arg Leu Glu Arg Arg Val
 290 295 300
 45 Ala Arg Glu Asp Thr Asp Ile Ala Gly Gln Arg Leu Pro Ala Gly Gly
 305 310 315 320
 Ser Val Val Ile Leu Val Ala Ala Val Asn Arg Ala Pro Val Ser Ala
 325 330 335
 50 Gly Ser Asp Ala Ser Thr Thr Val Pro His Ala Gly Gly Arg Pro Arg
 340 345 350
 55 Thr Ser Ala Pro Ser Val Pro Ser Ala Pro Phe Asp Leu Thr Arg Pro
 355 360 365
 60 Val Ala Ala Pro Gly Pro Phe Gly Leu Pro Gly Asp Leu His Phe Arg
 370 375 380

24/35

Leu Gly Gly Pro Leu Val Gly Thr Val Ala Glu Ala Ala Leu Gly Ala
 385 390 395 400
 5
 Leu Ala Ala Arg Leu Pro Gly Leu Arg Ala Ala Gly Pro Ala Val Arg
 405 410 415
 10
 Arg Arg Arg Ser Pro Val Leu His Gly His Ala Arg Leu Pro Val Ala
 420 425 430
 15
 Val Ala Arg Thr Ala Arg Asp Leu Pro Ala Thr Ala Pro Arg Asn
 435 440 445
 20
 <210> 14
 <211> 424
 <212> PRT
 <213> Streptomyces eurythermus
 <400> 14
 25
 Met Arg Ile Leu Leu Thr Ser Phe Ala His Asn Thr His Tyr Tyr Asn
 1 5 10 15
 30
 Leu Val Pro Leu Gly Trp Ala Leu Arg Ala Ala Gly His Asp Val Arg
 20 25 30
 35
 Val Ala Ser Gln Pro Ser Leu Thr Gly Thr Ile Thr Gly Ser Gly Leu
 35 40 45
 Thr Ala Val Pro Val Gly Asp Asp Thr Ala Ile Val Glu Leu Ile Thr
 50 55 60
 40
 Glu Ile Gly Asp Asp Leu Val Leu Tyr Gln Gln Gly Met Asp Phe Val
 65 70 75 80
 45
 Asp Thr Arg Asp Glu Pro Leu Ser Trp Glu His Ala Leu Gly Gln Gln
 85 90 95
 50
 Thr Ile Met Ser Ala Met Cys Phe Ser Pro Leu Asn Gly Asp Ser Thr
 100 105 110
 55
 Ile Asp Asp Met Val Ala Leu Ala Arg Ser Trp Lys Pro Asp Leu Val
 115 120 125
 60
 Leu Trp Glu Pro Phe Thr Tyr Ala Gly Pro Val Ala Ala His Ala Cys
 130 135 140
 Gly Ala Ala His Ala Arg Leu Leu Trp Gly Pro Asp Val Val Leu Asn

25/35

	145		150		155		160
5	Ala Arg Arg Gln Phe Thr Arg Leu Leu Ala Glu Arg Pro Val Glu Gln	165		170		175	
10	Arg Glu Asp Pro Val Gly Glu Trp Leu Thr Trp Thr Leu Glu Arg His	180		185		190	
15	Gly Leu Ala Ala Asp Ala Asp Thr Ile Glu Glu Leu Phe Ala Gly Gln	195		200		205	
20	Trp Thr Ile Asp Pro Ser Ala Gly Ser Leu Arg Leu Pro Val Asp Gly	210		215		220	
25	Glu Val Val Pro Met Arg Phe Val Pro Tyr Asn Gly Ala Ser Val Val	225		230		235	240
30	Pro Ala Trp Leu Ser Glu Pro Pro Ala Arg Pro Arg Val Cys Val Thr	245		250		255	
35	Leu Gly Val Ser Thr Arg Glu Thr Tyr Gly Thr Asp Gly Val Pro Phe	260		265		270	
40	His Glu Leu Leu Ala Gly Leu Ala Asp Val Asp Ala Glu Ile Val Ala	275		280		285	
45	Thr Leu Asp Ala Gly Gln Leu Pro Asp Ala Ala Gly Leu Pro Gly Asn	290		295		300	
50	Val Arg Val Val Asp Phe Val Pro Leu Asp Ala Leu Leu Pro Ser Cys	305		310		315	320
55	Ala Ala Ile Val His His Gly Gly Ala Gly Thr Cys Phe Thr Ala Thr	325		330		335	
60	Val His Gly Val Pro Gln Ile Val Val Ala Ser Leu Trp Asp Ala Pro	340		345		350	
65	Leu Lys Ala His Gln Leu Ala Glu Ala Gly Ala Gly Ile Ala Leu Asp	355		360		365	
70	Pro Gly Glu Leu Gly Val Asp Thr Leu Arg Gly Ala Val Val Arg Val	370		375		380	
75	Leu Glu Ser Arg Glu Met Ala Val Ala Ala Arg Arg Leu Ala Asp Glu	385		390		395	400

27/35

Gly Ala Thr Arg Ile Asp Val Asp Tyr Leu Val Gly Val Pro Gly Glu
 180 185 190

5 Gly Val Arg His Leu Lys Glu Thr His Arg Ile Thr Leu Phe Gly Arg
 195 200 205

10 Ala Gln Tyr Glu Ala Ala Phe Thr Ala Ala Gly Met Ser Val Glu Tyr
 210 215 220

15 Leu Pro His Ala Ala Thr Asp Arg Gly Leu Phe Val Gly Val Gln Ala
 225 230 235 240

20 <210> 16
 <211> 72
 <212> DNA
 <213> Artificial
 <220>
 <223> primer

25 <400> 16
 ggggaattca gatctgggtct agaggtcagc cggcgtggcg gcgcgtgagt tcctccagtc 60
 gcgggacgat ct 72

30 <210> 17
 <211> 38
 <212> DNA
 <213> Artificial

35 <220>
 <223> Primer

40 <400> 17
 gggcatatga acgaccgtcc ccgccgcgcc atgaaggg 38

45 <210> 18
 <211> 50
 <212> DNA
 <213> Artificial
 <220>
 <223> primer

50 <400> 18
 cccctctaga ggtcactgtg cccggctgtc ggccggcggcc ccgcgcatgg 50

55 <210> 19
 <211> 52
 <212> DNA
 <213> Artificial

60 <220>
 <223> primer

28/35

<400> 19
cccctctaga ggtcatgcgc gctccagttc cctgccgcc ggggaccgct tg 52

5
<210> 20
<211> 81
<212> DNA
<213> Artificial

10
<220>
<223> primer

<400> 20
15 ggggtctagat cgattaatta aggaggacat tcatgcgcgt cctgggtgacc ggaggtgcgg 60
gcttcatcgg ctgcacttc a 81

20
<210> 21
<211> 40
<212> DNA
<213> Artificial

25
<220>
<223> primer

<400> 21
30 gggcatatgt acgagggcgg gttcgccgag ctttacgacc 40

<210> 22
<211> 40
<212> DNA
35 <213> Artificial

<220>
<223> primer

40
<400> 22
ggggctctaga ggtcatccgc gcacaccgac gaacaaccgc 40

<210> 23
45 <211> 38
<212> DNA
<213> Artificial

<220>
50 <223> primer

<400> 23
gggcatatgg cggcgagcac tacgacggag gggaatgt 38

55
<210> 24
<211> 38
<212> DNA
<213> Artificial

50
<220>

29/35

<223> primer

<400> 24
5 gggctctagag gtcacgggtg gctcctgccg gccctcag 38

<210> 25
<211> 22
10 <212> DNA
<213> Artificial

<220>
<223> primer

15 <400> 25
catcgtcaag gagttcgacg gt 22

<210> 26
20 <211> 21
<212> DNA
<213> Artificial

<220>
25 <223> primer

<400> 26
gccagctcgg cgacgtccat c 21

30 <210> 27
<211> 35
<212> DNA
35 <213> Artificial

<220>
<223> primer

<400> 27
40 gggcatatga gccccgcacc cgccaccgag gaccc 35

<210> 28
<211> 42
45 <212> DNA
<213> Artificial

<220>
<223> primer

50 <400> 28
ggctctagagg tcagttccgc ggtgcggtgg cgggcaggtc ac 42

<210> 29
55 <211> 41
<212> DNA
<213> Artificial

50 <220>
<223> primer

30/35

5 <400> 29
gggcatatgc gtatcctgct gacgtcggtc gcgcacaaca c 41

<210> 30
<211> 44
<212> DNA
<213> Artificial

10 <220>
<223> primer

15 <400> 30
ggtctagagg tcaggcgcg gggcgcgcg cggtgagggc ttcg 44

20 <210> 31
<211> 39
<212> DNA
<213> Artificial

25 <220>
<223> primer

<400> 31
ggagatctgg cgcggcggtg cgcggcggtg aggcgttcg 39

30 <210> 32
<211> 42
<212> DNA
<213> Artificial

35 <220>
<223> primer

40 <400> 32
gggcatatga acctcgaata cagcggcgac atcgcccggt tg 42

45 <210> 33
<211> 44
<212> DNA
<213> Artificial

<220>
<223> primer

50 <400> 33
ggtctagagg tcaggcctgg acgccgacga agagtcgcg gtcg 44

55 <210> 34
<211> 37
<212> DNA
<213> Artificial

60 <220>
<223> primer

31/35

<400> 34
gggcatatga ctacctacgt ctgggactac ctggcg
37

5 <210> 35
<211> 40
<212> DNA
<213> Artificial

10 <220>
<223> primer

<400> 35
15 ggtctagagg tcagagcgtg gccagtacct cgtgcagggc 40

<210> 36
<211> 41
<212> DNA
20 <213> Artificial

<220>
<223> primer

25 <400> 36
gggcatatgg tgaacgatcc gatgccgcgc ggcagtggca g 41

<210> 37
30 <211> 43
<212> DNA
<213> Artificial

<220>
35 <223> primer

<400> 37
ggtctagagg tcaacctcca gagtgtttcg atgggggtggt ggg 43

40 <210> 38
<211> 39
<212> DNA
45 <213> Artificial

<220>
<223> primer

<400> 38
50 gggcatatga agggcatcat cctggcgggc ggcagcggc 39

<210> 39
<211> 46
55 <212> DNA
<213> Artificial

<220>
<223> primer

60 <400> 39

32/35

gggtctagagg tcatgcggcc ggtccggaca tgagggtctc cgccac

46

5 <210> 40
<211> 36
<212> DNA
<213> Artificial

10 <220>
<223> primer

<400> 40
gggcatatgc ggctgctggt caccggaggt gcgggc

36

15 <210> 41
<211> 36
<212> DNA
<213> Artificial

20 <220>
<223> primer

25 <400> 41
gggtctagagg tcagtcggtg cgcggggcct cctgcg

36

30 <210> 42
<211> 40
<212> DNA
<213> Artificial

35 <220>
<223> primer

<400> 42
gggcataatgt gtcctcctta attaatcgat gcgttcgtcc

40

40 <210> 43
<211> 51
<212> DNA
<213> Artificial

45 <220>
<223> primer

<400> 43
ggagatctgg tctagatcgt gttccctcc ctgcctcgtg gtccctcacg c

51

50 <210> 44
<211> 36
<212> DNA
<213> Artificial

<220>
<223> primer

0 <400> 44
gggcatatga gcacccttc cgcaccacc gttccg

36

5 <210> 45
<211> 40
<212> DNA
<213> Artificial

10 <220>
<223> primer

<400> 45
ggtctagagg tcagttacagc gtgtgggcac acgcccaccag 40

15 <210> 46
<211> 37
<212> DNA
<213> Artificial

20 <220>
<223> primer

<400> 46
gggcatatga gcagttctgt cgaagctgag gcaagtg 37

25 <210> 47
<211> 41
<212> DNA
<213> Artificial

30 <220>
<223> primer

35 <400> 47
ggtctagagg tcatcgcccc aacgcccaca agctatgcag g 41

40 <210> 48
<211> 33
<212> DNA
<213> Artificial

45 <220>
<223> primer

<400> 48
cccatatgac cggagttcga ggtacgcggc ttg 33

50 <210> 49
<211> 33
<212> DNA
<213> Artificial

55 <220>
<223> primer

60 <400> 49
gatactagtc cgccgaccgc acgtcgctga gcc 33

5 <210> 50
<211> 38
<212> DNA
<213> Artificial

<220>
<223> primer

10 <400> 50
tgcactagtg gccgggcgct cgacgtcatc gtcgacat 38

15 <210> 51
<211> 36
<212> DNA
<213> Artificial

<220>
20 <223> primer

<400> 51
tcgatatcgt gtctctggcggt ttcacctgca acgctg 36

25 <210> 52
<211> 36
<212> DNA
<213> Artificial

30 <220>
<223> primer

<400> 52
35 ggtctagact acgccgactg cctcggcgag gagccc 36

40 <210> 53
<211> 36
<212> DNA
<213> Artificial

<220>
<223> primer

45 <400> 53
ggcatatggt cgccgacgtg gaaacgacct gctgcg 36

50 <210> 54
<211> 35
<212> DNA
<213> Artificial

55 <220>
<223> primer

<400> 54
60 ggaattcggc caggacgcgt ggctggtcac cggct 35

35/35

5 <210> 55
<211> 42
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 55
10 ggtctagaaa gagcgtgagc aggctcttct acagccaggt ca 42

<210> 56
<211> 38
15 <212> DNA
<213> Artificial

<220>
<223> primer
20

<400> 56
ggcatgcagg aaggagagaa ccacgatgac caccgacg 38

25 <210> 57
<211> 41
<212> DNA
<213> Artificial

30 <220>
<223> primer

<400> 57
35 ggtctagaca ccagcgtat cctttctcgg ttctctttgt g 41